

SEARCH REQUEST FORM

Scientific and Technical Information Center

CRFE

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 8/25/02
 Art Unit: 1635 Phone Number 306-5220 Serial Number: 09/522,278
 Mail Box and Bldg/Room Location: 11D03 Results Format Preferred (circle): PAPER DISK E-MAIL

11e12
 If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Delivery of Substances to Cells

Inventors (please provide full names): O'Hare et al.

Earliest Priority Filing Date: 2/14/01

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search Sig ID No 12

Sig limited to 50 AA

Unlimited search

Edward Han
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Interference + Regular
 Data Bases
 Thanks.

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>2</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>8/28/02</u>	Bibliographic _____	Dr.Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <u>✓</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: August 28, 2002, 12:23:41 : Search time 30.25 seconds

(Without alignments)
(1721.371 Million cell updates/sec)

Title: US-09-522-278b-12

Perfect score: 1561

Sequence: 1 MTRSRVSKSGPREVPRDEYE.....PTERRAPARSASRRPRVPE 301

Scoring table: BLOSUM62

Gapped 10.0, Gapped 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:.*
2: SP-bacteria:.*
3: SP-fungi:.*
4: SP-human:.*
5: SP-invertebrate:.*
6: SP-mammal:.*
7: SP-mhc:.*
8: SP-organellar:.*
9: SP-phage:.*
10: SP-plant:.*
11: SP-rodent:.*
12: SP-virus:.*
13: SP-vertebrate:.*
14: SP-vertebrate:.*
15: SP-virus:.*
16: SP-bacterioph:.*
17: SP-archaeal:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1014.5	65.0	300	12 P89468	P89468 herpes simp
2	270.5	17.3	304	12 O39253	O39253 equine herp
3	228	14.6	301	12 O9E306	O9E306 cercopithec
4	210	13.5	249	12 O69318	O69318 marek's dis
5	210	13.5	249	12 O9E6M7	O9E6M7 turkey herp
6	207	13.3	241	12 O89247	O89247 gallid herp
7	198	12.7	283	12 O9DH2	O9DH2 meleagrid h
8	168.5	10.8	388	12 O9NY42	O9NY42 homo saplen
9	168.5	10.8	441	4 O75685	O75685 homo saplen
10	153	9.8	252	12 O9DMG9	O9DMG9 rat cyomeg
11	149.5	9.6	956	4 O9UQ35	O9UQ35 homo saplen
12	149.5	9.6	2752	4 O9UQ35	O9UQ35 herpes simp
13	149.5	9.6	3122	12 P89459	P89459 gallid herp
14	148	9.5	266	12 O56868	O56868 delnococtus
15	146.5	9.4	395	16 O9RVT4	O9RVT4 delnococtus
16	146.5	9.4	1343	4 O9H7M4	O9H7M4 homo saplen

17	146	9.4	839	16 O9RX57	O9RX57 delnococtus
18	146	9.4	1262	4 O9UQ40	O9UQ40 homo saplen
19	144	9.2	1037	16 O9AC25	O9AC25 caulobacter
20	144	9.2	1201	10 O9CGS1	O9CGS1 arabidopsis
21	143.5	9.2	889	4 O9UL51	O9UL51 homo saplen
22	143.5	9.2	1154	4 O9P2P0	O9P2P0 homo saplen
23	142	9.1	1249	5 O9N8C4	O9N8C4 typanosoma
24	140.5	9.0	1265	3 O9S920	O9S920 pneumocysti
25	140.5	9.0	1592	3 O9P6T1	O9P6T1 neurospora
26	140	9.0	1132	16 O9RRC7	O9RRC7 delnococtus
27	139.5	8.9	932	5 O93562	O93562 caenorhabdl
28	139	8.9	438	16 O9AZM5	O9AZM5 caulobacter
29	138.5	8.9	1312	4 O9N859	O9N859 homo saplen
30	137	8.8	590	2 O9S205	O9S205 streptomyce
31	137	8.8	797	2 O9RKS9	O9RKS9 streptomyce
32	137	8.8	835	2 O9K3E2	O9K3E2 streptomyce
33	137	8.8	1069	12 O69140	O69140 human herpe
34	136.5	8.7	694	6 O9GK7	O9GK7 oryctolagus
35	136.5	8.7	889	4 O9US82	O9US82 homo saplen
36	136.5	8.7	1320	11 O08784	O08784 mus musculu
37	136	8.7	212	11 O70446	O70446 mus musculu
38	136	8.7	436	4 O9S01	O9S01 homo saplen
39	136	8.7	2936	5 O9NKP7	O9NKP7 leishmania
40	135.5	8.7	612	2 O92614	O92614 streptomyce
41	135.5	8.7	1175	6 O9TV66	O9TV66 oryctolagus
42	134	8.6	667	11 O9RID9	O9RID9 mus musculu
43	134	8.6	721	4 O9E648	O9E648 homo saplen
44	134	8.6	737	11 O9WVF3	O9WVF3 mus musculu
45	134	8.6	806	11 O9WVF4	O9WVF4 mus musculu

ALIGNMENTS

RESULT 1
P89468 PRELIMINARY: PRT: 300 AA.
AC P89468: 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TEGUMENT PROTEIN.
GN U149.
OS Herpes simplex virus (type 2).
OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae:
OC Alphaherpesvirinae: Simplexvirus.
OK NCBI_TaxID=10310;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HG52:
RX MEDLINE=87111457; PubMed=3027242;
RA McGeoch D.J., Moss H.W., McNab D., Frame M.C.:
RT "DNA sequence and genetic content of the HindIII 1 region in the short
RT unique component of the herpes simplex virus type 2 genome:
RT identification of the gene encoding glycoprotein G, and evolutionary
RT comparisons.";
RL J. Gen. Virol. 68:19-38(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-HG52:
RX MEDLINE=90278430; PubMed=2161906;
RA Everett R., Fenwick M.:
RT "Comparative DNA sequence analysis of the host shut-off genes of
RT different strains of herpes simplex virus: type 2 strain HG52 encodes
RT a truncated UL1 product.";
RL J. Gen. Virol. 71:1387-1390(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-HG52:
RX MEDLINE=92113549; PubMed=1662697;
RA McGeoch D.J., Cunningham C., McIntyre G., Dolan A.:
RT "Comparative sequence analysis of the long repeat regions and
RT adjoining parts of the long unique regions in the genomes of herpes